

## **Studies on the population genetic structure of green turtles (*Chelonia mydas*) nesting and foraging in the northwestern Pacific**

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The green turtle (*Chelonia mydas*) has a circumglobal distribution, occurring throughout tropical and, to a lesser extent, subtropical waters, and is listed as Endangered (EN) by the International Union for the Conservation of Nature and Natural Resources (IUCN 2013). It arose as an ancient species about 34 million years ago (Naro-Maciel et al. 2008) and is one of the extant species that has survived several large-scale climatic and sea level changes (Hamann et al. 2007). However, there is little fossil evidence to indicate how populations of existing marine turtle species may have changed or how they coped with past climate change (Hamann et al. 2007; Hawkes et al. 2009). In addition, their migratory nature and long generation time make it difficult to know their detail life history and to plan for the conservation strategies. In the present study, the genetic structures of the green turtles' nesting populations and foraging aggregations in the northwestern Pacific region were analyzed in order to clarify their population history and foraging ecology in this region.

### **Chapter 1: Genetic structure of green turtle peripheral populations nesting in the northwestern Pacific rookeries**

Several green turtle nesting populations have been reported in the northwestern Pacific region, the northernmost limit of its distribution range. However, the population history in this region as a whole is not well understood. To clarify how the green turtle nesting populations have been formed in the northwestern Pacific region, the genetic compositions of mitochondrial DNA (mtDNA) control region sequences in the northwestern Pacific were compared with that of the other Pacific populations. A total of 302 samples were analyzed from the northwestern Pacific rookeries, including 78 newly collected samples from rookeries in the Ryukyu Archipelago, Japan. The present results revealed that the northwestern Pacific populations consisted of one highly endemic lineage (Clade IV) in the northwestern Pacific rookeries and two other lineages (Clade I and V) which were widely observed in other Pacific populations. It was concluded that the highly endemic lineage was derived from a refugial population survived in the northwestern Pacific during the Last Glacial Maximum, and that the other two lineages were colonized from populations at lower latitudes during interglacial periods. The green turtle nesting populations in the present periphery of their distribution range had been thought to have their origin in colonization from lower latitudes, which served as refugia during glacial periods. However, the present results indicated that the northwestern Pacific peripheral populations have been maintained in the glacial periods.

## **Chapter 2: Size and genetic compositions of green turtles in the foraging aggregations along the Japanese coasts**

Since the migratory green turtles exhibit ontogenetic habitat shifts during their life, the individuals occupying a habitat may come from different origin depending on their size. In this chapter, first the size compositions of green turtles were examined in two foraging grounds in the Yaeyama Group around southern Ryukyus and the Cape Muroto in western Japanese main islands. The size compositions of the former and the latter showed a near unimodal distribution and a bimodal distribution, respectively. Next the mixed stock analyses by the mtDNA haplotypes were conducted for three size classes in three regional foraging grounds (Yaeyama, Okinawa and western Japanese main islands) in order to estimate which green turtle rookeries contribute to the each size class of foraging grounds. The estimations showed that the Yaeyama and Okinawa foraging grounds were sourced various rookeries in the Indo-Pacific region in all size classes. In contrast, the most turtles foraging in the western Japanese main islands were sourced from Japanese rookeries of the Ogasawara Group and central Ryukyus in all size classes. Although statistically significant shifts in haplotype compositions were not observed among size classes within each foraging ground, there were subtle differences in the frequencies of the rookery contributions among size classes of the Yaeyama foraging ground. Both the variation of the frequencies of the rookery contributions and the bimodal size distribution indicate that the foraging aggregations are not static. Therefore, it was suggested that although the foraging aggregations were apparently balanced, recruitments are likely to be complex and dynamic processes.

The present results have new implications for the conservation of green turtles in the northwestern Pacific region. The findings in chapter 1 indicated that the northwestern Pacific populations had not only high genetic diversity but also phylogenetic endemism, and highlight the evolutionary significance of these populations. Therefore, it is important to treat nesting green turtles in this region as a long-term conservation resource for planning and practice of conservation strategies. However, the results in chapter 2 highlight that the concentrative conservation by selecting foraging grounds along the Japanese coasts would not produce the hopeful effects, because the turtles clearly shift their foraging habitats as they mature.

The present study first investigated whether the rookery origins could change depending on the size classes in the foraging grounds of the northwestern Pacific. Future continual monitoring both on the size and genetic composition of each foraging ground will advance our knowledge of the habitat shifts of green turtles in this region and provide us useful information for planning the effective conservation strategies.